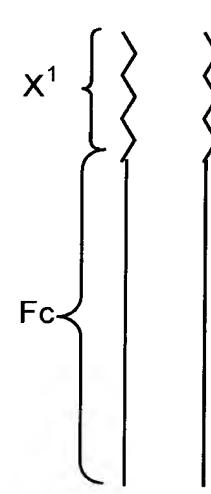
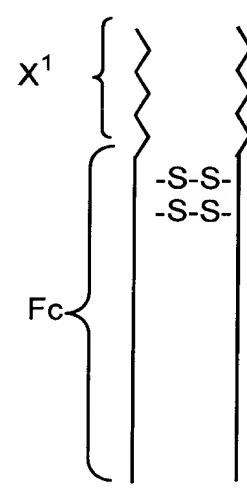
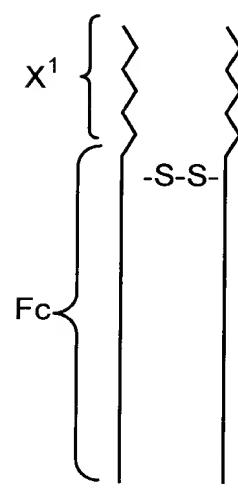
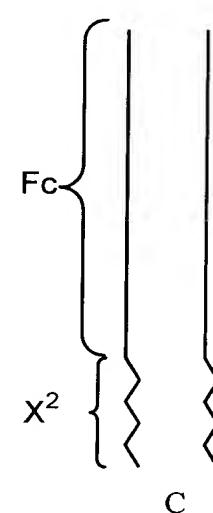
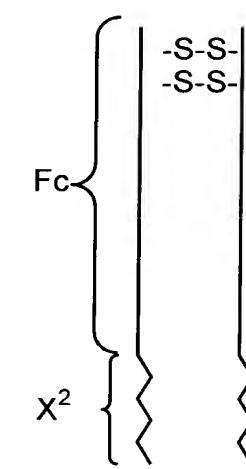
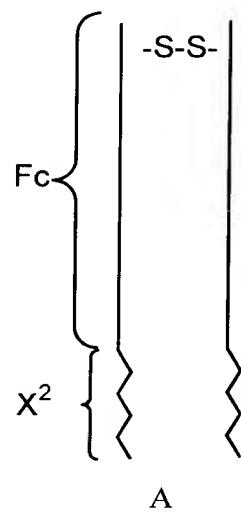


FIGURE 1



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FIGURE 2

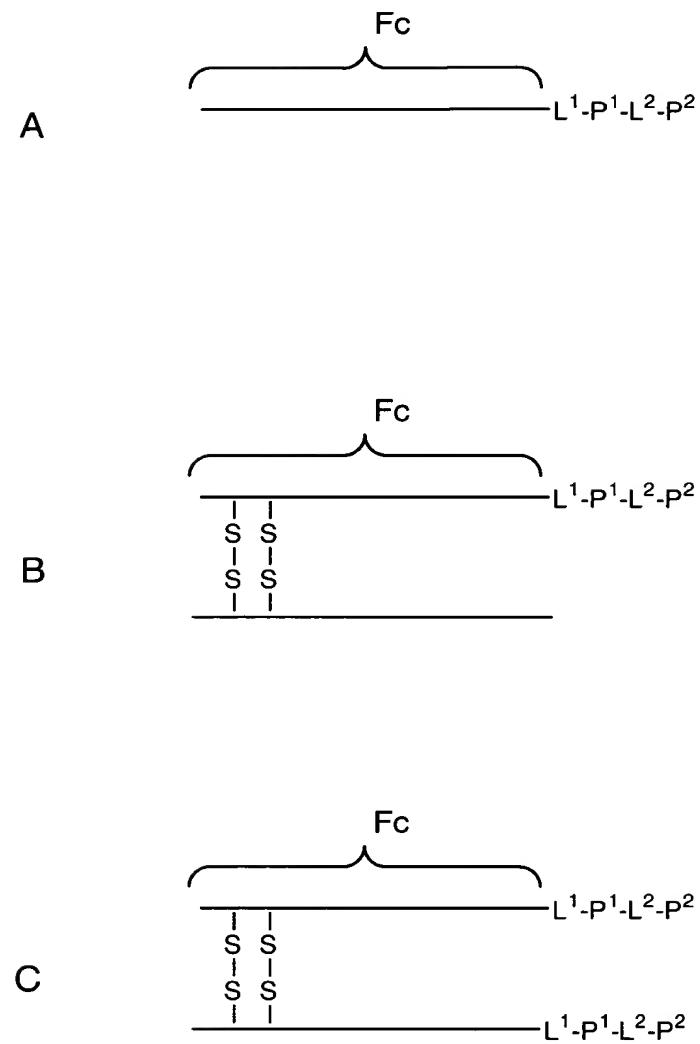


FIGURE 3A

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ATGGACAAA ACTCACACATGTCCACCTTGTCAGCTCCGGAACTCCTGGGGGACCGTCA
 1 -----+-----+-----+-----+-----+-----+-----+-----+ 60
 TACCTGTTTGAGTGTACAGGTGGAACAGGTGAGGCCCTGAGGACCCCCCTGGCAGT

 a M D K T H T C P P C P A P E L L G G P S -

 GTCTTCCTCTTCCCCCAAACCCAAGGACACCCTCATGATCTCCGGACCCCTGAGGTC
 61 -----+-----+-----+-----+-----+-----+-----+-----+ 120
 CAGAAGGAGAAGGGGGTTTGGGTTCCGTGGAGTACTAGAGGGCTGGGACTCCAG

 a V F L F P P K P K D T L M I S R T P E V -

 ACATGCGTGGTGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTG
 121 -----+-----+-----+-----+-----+-----+-----+-----+ 180
 TGTAACGCACCACCACTGCACTCGGTGCTTCTGGACTCCAGTTCAAGTTGACCATGCAC

 a T C V V V D V S H E D P E V K F N W Y V -

 GACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACG
 181 -----+-----+-----+-----+-----+-----+-----+-----+ 240
 CTGCGCACCTCCACGTATTACGGTTCTCGGCCCTCCTCGTCATGTTGCTGTC

 a D G V E V H N A K T K P R E E Q Y N S T -

 TACCGTGTGGTCAGCGTCTCACCGTCTGCACCAGGACTGGCTGAATGGCAAGGAGTAC
 241 -----+-----+-----+-----+-----+-----+-----+-----+ 300
 ATGGCACACCACTCGCAGGAGTGGCAGGACGTGGCTCTGACCGACTTACCGTTCTCATG

 a Y R V V S V L T V L H Q D W L N G K E Y -

 AAGTGCAGGTCTCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCCTCCAAAGCC
 301 -----+-----+-----+-----+-----+-----+-----+-----+ 360
 TTACGTTCCAGAGGTTGTTGGGAGGGTCGGGGTAGCTCTTTGGTAGAGGTTCCGG

 a K C K V S N K A L P A P I E K T I S K A -

 AAAGGGCAGCCCCGAGAACACAGGTGTACACCCTGCCCTATCCCAGGATGAGCTGACC
 361 -----+-----+-----+-----+-----+-----+-----+-----+ 420
 TTTCCCGTCGGGCTTGGTGTCCACATGTGGGACGGGGTAGGGCCCTACTCGACTGG

 a K G Q P R E P Q V Y T L P P S R D E L T -

 AAGAACCCAGGTCAAGCCTGACCTGCCCTGGCAAAGGCTTCTATCCCAGCGACATGCCGTG
 421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
 TTCTTGGTCCAGTCGGACTGGACGGACCAAGTTCGAAAGATAGGGTCGCTGTAGCGGCAC

 a K N Q V S L T C L V K G F Y P S D I A V -

 GAGTGGGAGAGCAATGGCAGCCGGAGAACAACTACAAGACCAAGCCCTCCGTGCTGGAC
 481 -----+-----+-----+-----+-----+-----+-----+-----+ 540
 CTCACCCCTCTCGTACCCGTCGGCTCTGGTATGTTCTGGTGCAGGGCACGACCTG

 a E W E S N G Q P E N N Y K T T P P V L D -

 TCCGACGGCTCCTCTTCCCTACAGCAAGCTACCGTGGACAAGAGCAGGTGGCAGCAG
 541 -----+-----+-----+-----+-----+-----+-----+-----+ 600
 AGGCTGCCAGGAAGAACAGGAGATGTCGTTGAGTGGCACCTGTTCTCGTCCACCGTCG

 a S D G S F F L Y S K L T V D K S R W Q Q -

 GGGAACGTCTTCATGCTCCGTGATGCATGAGGCTCTGCACAACCAACTACACGAGAAC
 601 -----+-----+-----+-----+-----+-----+-----+-----+ 660
 CCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTATGCGTCTTC

 a G N V F S C S V M H E A L H N H Y T Q K -

BY CLAUDIO GUERRA
ETC DATA

FIGURE 3B

AGCCTCTCCCTGTCTCCGGTAAA
661 -----+-----+---- 684
TCGGAGAGGGACAGAGGCCATT
a S L S L S P G K

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